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SEQUENCE LISTING

<110> Rauch, Charles
Walczak, Henning

<120> RECEPTOR THAT BINDS TRAIL

<130> 2625-E

<140> US 09/378,045
<141> 1999-08-20

<150> US 08/883,036
<151> 1997-06-26

<150> US 08/869,852
<151> 1997-06-04

<150> US 08/829,536
<151> 1997-03-28

<150> US 08/815,255
<151> 1997-03-12

<150> US 08/799,861
<151> 1997-02-13

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<170> PatentIn version 3.0/ Microsoft Word, Version 6.0.1

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Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
1               5                   10                  15

agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ccc       96
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
            20                  25                  30

cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg      144
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
        35                  40                  45
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gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag      192
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
    50                  55                  60

cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg      240
Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
65                  70                  75                  80

tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc      288
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
                85                  90                  95

tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc      336
Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
            100                 105                 110

tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccg      384
Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
        115                 120                 125

tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc      432
Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
    130                 135                 140

cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca ggg tgt      480
Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
145                 150                 155                 160

ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc      528
Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
                165                 170                 175

gaa tgt gtc cac aaa gaa tca ggt aca aag cac agt ggg gaa gcc cca      576
Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro
            180                 185                 190

gct gtg gag gag acg gtg acc tcc agc cca ggg act cct gcc tct ccc      624
Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro
        195                 200                 205

tgt tct ctc tca ggc atc atc ata gga gtc aca gtt gca gcc gta gtc      672
Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
    210                 215                 220

ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg aag aaa gtc      720
Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val
225                 230                 235                 240

ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg gac cct gag      768
Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu
                245                 250                 255

cgt gtg gac aga agc tca caa cga cct ggg gct gag gac aat gtc ctc      816
Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu
            260                 265                 270

aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct gag cag gaa      864
Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu
        275                 280                 285
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atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac atg ttg tcc      912
Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
    290                 295                 300

ccc ggg gag tca gag cat ctg ctg gaa ccg gca gaa gct gaa agg tct      960
Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser
305                 310                 315                 320

cag agg agg agg ctg ctg gtt cca gca aat gaa ggt gat ccc act gag     1008
Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu
                325                 330                 335

act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc ttt gac     1056
Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp
            340                 345                 350

tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat gag ata     1104
Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile
        355                 360                 365

aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg tac acg     1152
Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr
    370                 375                 380

atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc tct gtc cac     1200
Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His
385                 390                 395                 400

acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt gcc aag cag     1248
Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln
                405                 410                 415

aag att gag gac cac ttg ttg agc tct gga aag ttc atg tat cta gaa     1296
Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu
            420                 425                 430

ggt aat gca gac tct gcc atg tcc taa                                 1323
Gly Asn Ala Asp Ser Ala Met Ser
        435                 440


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<213>  Homo sapiens


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Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
1               5                   10                  15

Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
            20                  25                  30

Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
        35                  40                  45

Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
    50                  55                  60
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```
Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
65                  70                  75                  80

Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
                85                  90                  95

Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
            100                 105                 110

Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
        115                 120                 125

Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
    130                 135                 140

Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
145                 150                 155                 160

Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
                165                 170                 175

Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro
            180                 185                 190

Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro
        195                 200                 205

Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
    210                 215                 220

Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val
225                 230                 235                 240

Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu
                245                 250                 255

Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu
            260                 265                 270

Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu
        275                 280                 285

Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
    290                 295                 300

Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser
305                 310                 315                 320

Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu
                325                 330                 335

Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp
            340                 345                 350

Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile
        355                 360                 365

Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr
    370                 375                 380
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Sub B' cont

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Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His
385                 390                 395                 400

Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln
                405                 410                 415

Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu
            420                 425                 430

Gly Asn Ala Asp Ser Ala Met Ser
        435                 440


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   Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro
   1               5                  10                  15

ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat       95
Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn
                20                  25                  30

gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg      143
Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
            35                  40                  45

tnc acn atg ctg at                                                  157
Xaa Thr Met Leu
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Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe
1               5                  10                  15

Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu
            20                  25                  30

Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Xaa
        35                  40                  45

Thr Met Leu
    50
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